

FIG. 1

BsF(ab')₂
CHEMICALLY COUPLED
RODENT FRAGMENTS

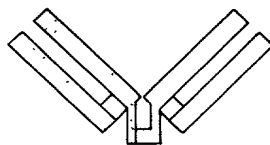


FIG. 2A

BsF(ab')₂
CHEMICALLY COUPLED
E. coli DERIVED FRAGMENTS

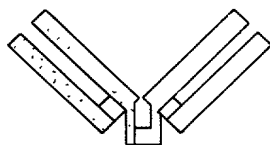


FIG. 2B

BsF(ab')₂
LEUCINE ZIPPER
ASSEMBLED

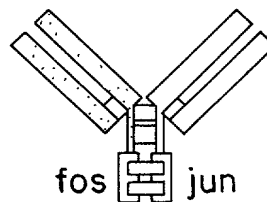
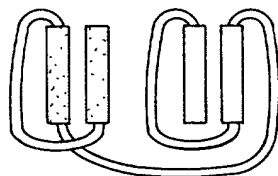
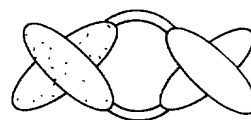


FIG. 2C



sFv DIMER

FIG. 2E



DIABODY

FIG. 2D

RECEPTOR

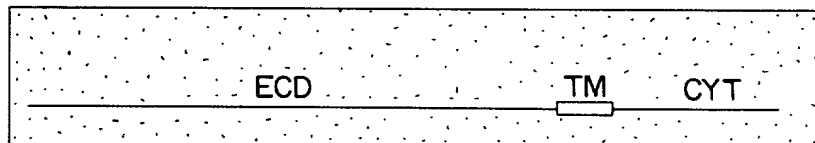


FIG. 3A

IgG1- HEAVY CHAIN

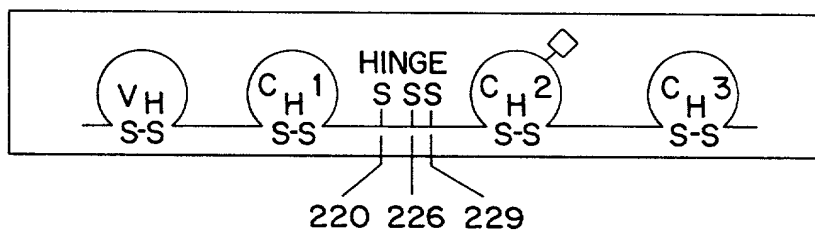


FIG. 3B

IMMUNOADHESIN

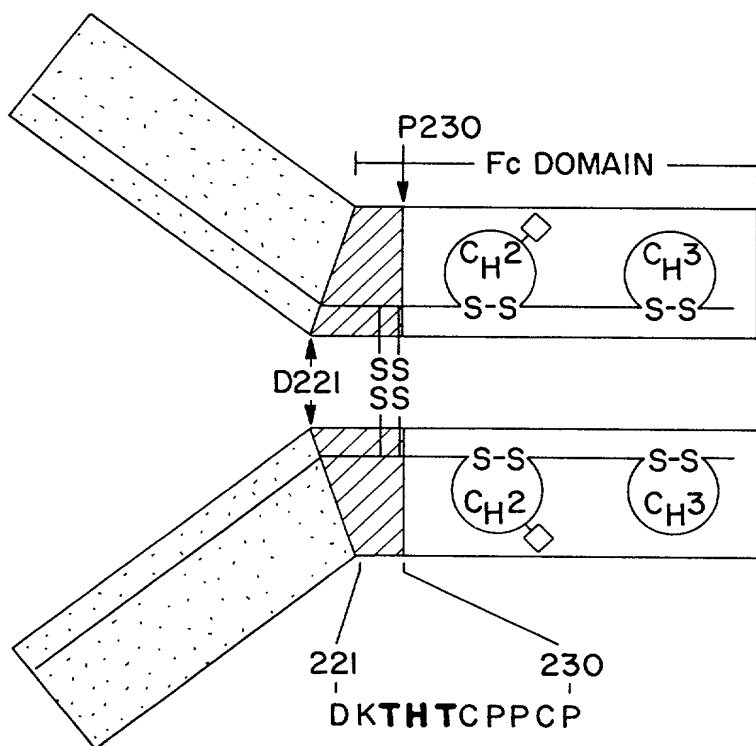
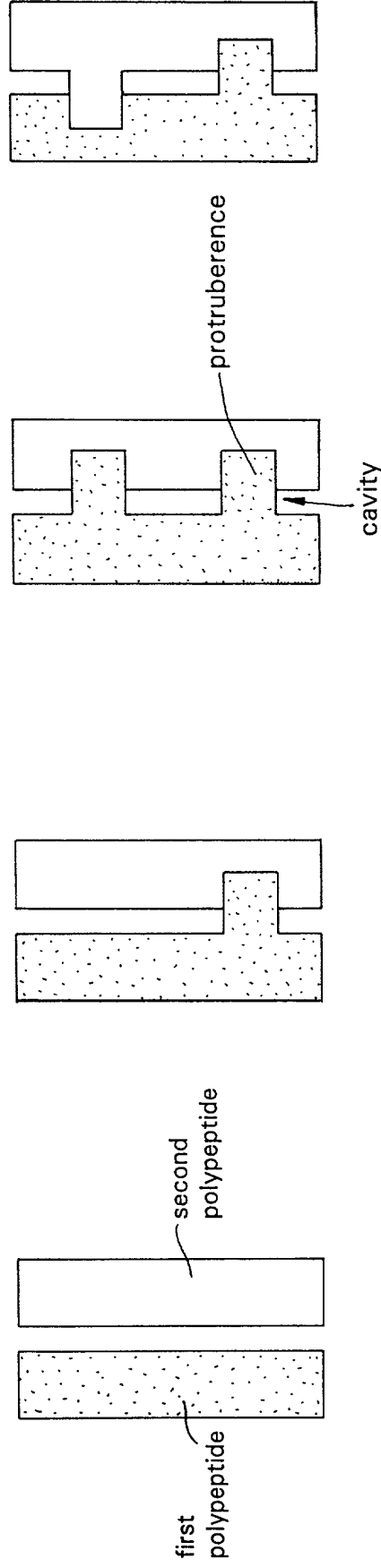


FIG. 3C



double mutants

double mutants

single mutants

Wild

Type

FIG. 4

Chen et al. • *CaMKII α Regulates the Activity of Ca^{2+} Channels*

[illegible]

middle, interface

exterior

	B	I	B	I	B	i							B	B	B							
IgG	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N
IgA	V	T	L	T	C	L	A	R	G	F	S	P	K	D	V	L	V	R	W	L	Q	G
IgD	S	W	L	L	C	E	V	S	G	F	S	P	P	N	I	L	L	M	W	L	ED	Q
IgE	R	T	L	A	C	L	I	Q	N	F	M	P	E	D	I	S	V	Q	W	L	H	N
IgM	T	K	L	T	C	L	V	T	D	L	T	T	Y	BSV	T	I	S	W	T	R	Z	
							370										380					

edge, interface

	I	i	I
IgG	D - G Q P E N N Y K T T P P V/M L D S D G S		
IgA	S Q E L P R E K Y L T W A S R Q Z PSQGTTT		
IgD	R E V N T S G F A P A R P P P Q P G S T T		
IgE	E V Q L P D A R H S T T Q P R K T K G S G		
IgM	D - - G E A V K T H T B I S Z S H P B A T		
	390		400

middle, interface

exterior

	B	I	B	I	B	I	B	i	B		B		B		B		B		B						
IgG	F	F	L	Y	S	K/R	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M
IgA	F	A	V	T	S	I	L	R	V	A	A	E	D	W	K	K	G	D	T	F	S	C	M	V	G
IgD	F	W	A	W	S	V	L	R	V	P	A	P	P	S	P	Q	P	A	T	Y	T	C	V	V	S
IgE	F	F	V	F	S	R	L	E	V	T	R	A	E	W	E	Q	K	D	E	F	I	C	R	A	V
IgM	F	S	A	V	G	E	A	S	I	C	E	B	B	W	B	S	G	E	R	F	T	C	T	V	T
							410									420									

exterior

[illegible]

FIG. 5

				EDGE				MIDDLE			
				↓				↓			
hIgG1	361	G	-	Q	P	R	E	P	Q	V	L
hIgG2		G	-	Q	P	R	E	P	Q	V	L
hIgG3		G	-	Q	P	R	E	P	Q	V	L
hIgG4		G	-	Q	P	R	E	P	Q	V	L
				↓				↓			
mIgG1	361	G	-	R	P	K	A	P	Q	V	L
mIgG2A		G	-	P	V	R	A	P	Q	V	L
mIgG2B		G	-	L	V	R	A	P	Q	V	L
mIgG3		G	-	R	A	Q	T	P	Q	V	L
				↓				↓			
hIgG1	400	L	V	K	G	F	Y	P	S	D	-
hIgG2		L	V	K	G	F	Y	P	S	D	-
hIgG3		L	V	K	G	F	Y	P	S	D	-
hIgG4		L	V	K	G	F	Y	P	S	D	-
				↓				↓			
mIgG1	410	M	I	T	D	F	F	P	E	D	I
mIgG2A		M	I	T	G	F	F	P	A	E	I
mIgG2B		L	V	V	G	F	F	P	G	D	I
mIgG3		L	V	T	N	F	F	P	S	E	I
				↓				↓			
hIgG1	410	L	V	K	G	F	Y	P	S	D	-
hIgG2		L	V	K	G	F	Y	P	S	D	-
hIgG3		L	V	K	G	F	Y	P	S	D	-
hIgG4		L	V	K	G	F	Y	P	S	D	-
				↓				↓			
mIgG1	410	M	I	T	D	F	F	P	E	D	I
mIgG2A		M	I	T	G	F	F	P	A	E	I
mIgG2B		L	V	V	G	F	F	P	G	D	I
mIgG3		L	V	T	N	F	F	P	S	E	I

FIG.6A

				EDGE				MIDDLE				450			
				↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG1	T	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG2	T	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG3	T	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG4	T	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG1	N	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG2A	N	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG2B	B	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG3	N	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
*****				*****				*****				*****			
451				460				470				480			
hIgG1	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgE	K	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG2	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG3	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
hIgG4	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG1	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG2A	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG2B	T	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
mIgG3	G	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
*****				*****				*****				*****			

FIG. 6B

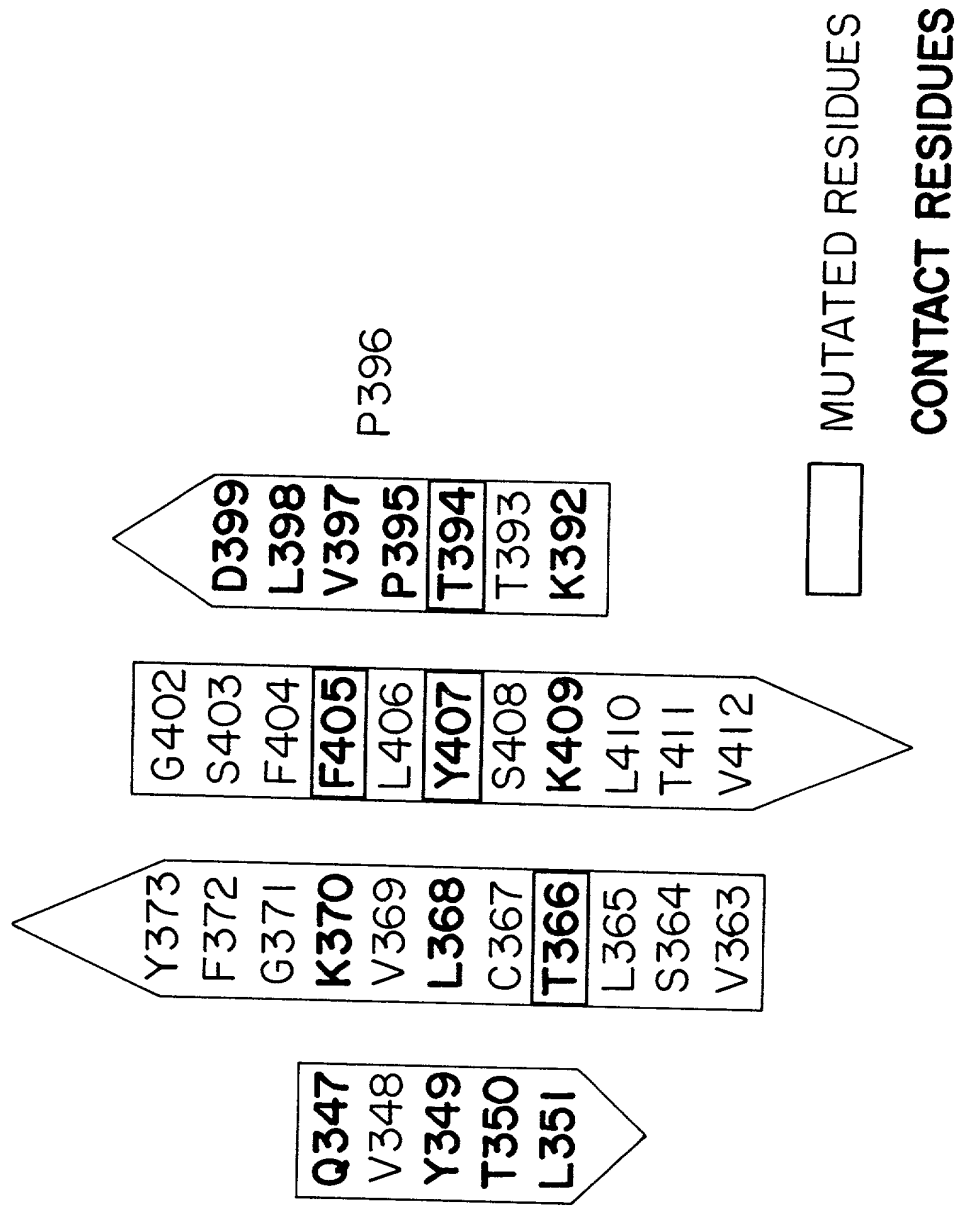


FIG. 7

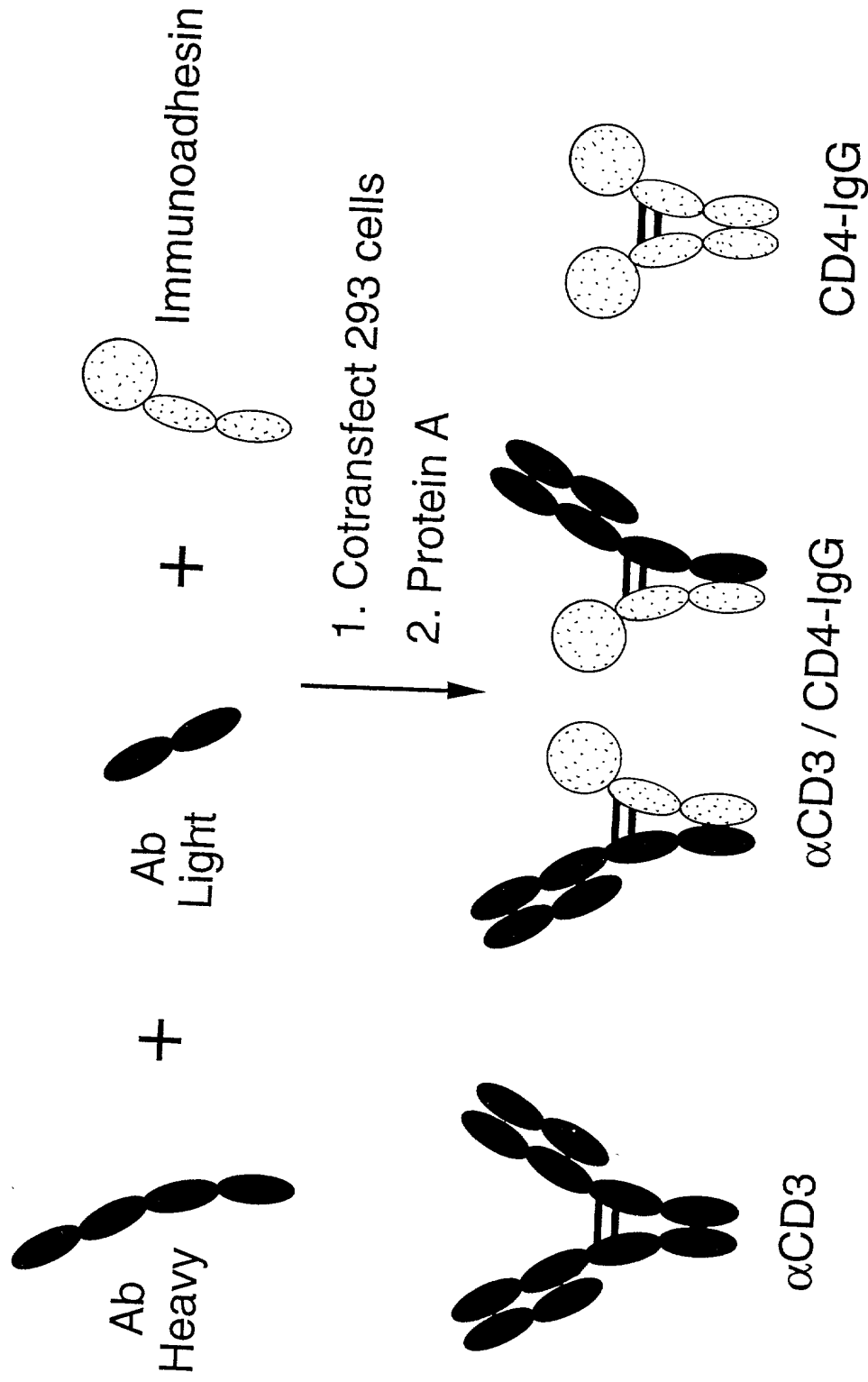


FIG. 8

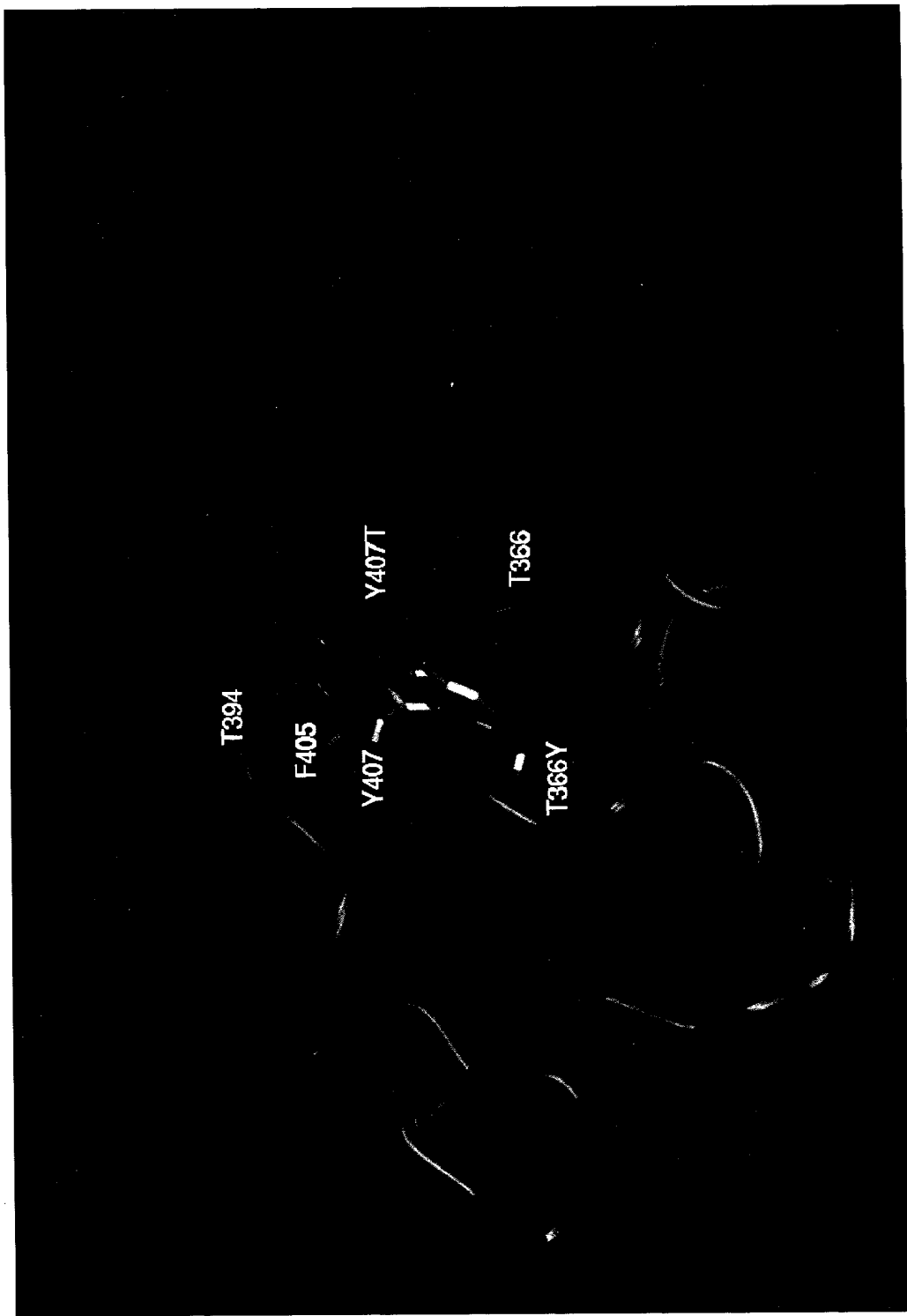
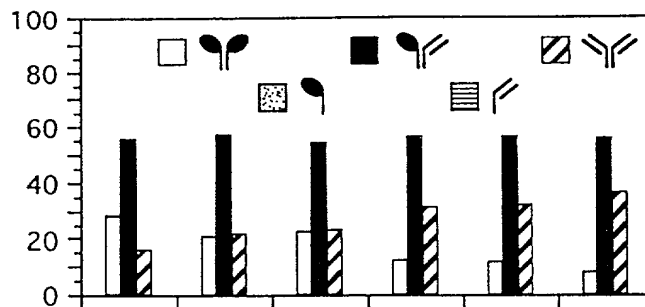


FIG. 9

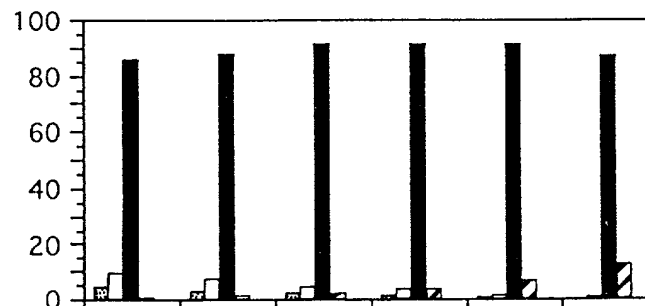
FIG.10A



Ab/Ia

WT/WT

FIG.10B



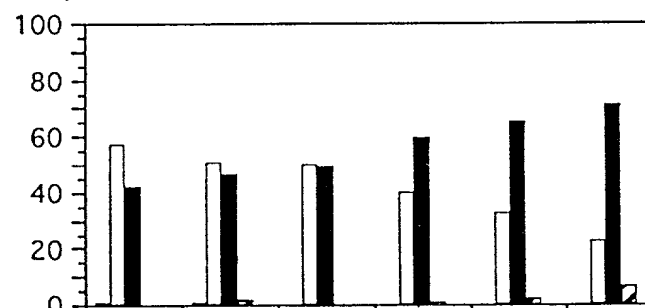
Y407T/T366Y

FIG.10C



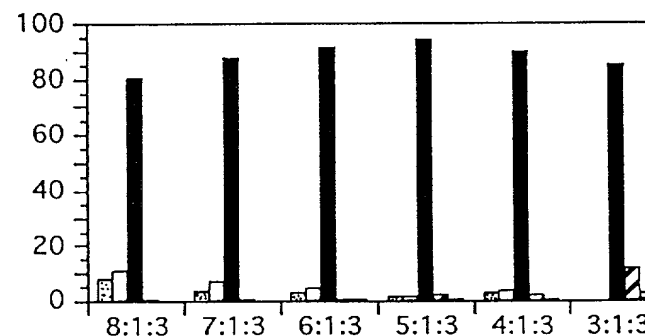
T366Y/Y407T

FIG.10D



F405A/T394W

FIG.10E



T366Y:F405A/
T394W:Y407T

Ratio of Input DNA: IA : H : L